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PAGE: 1

RAW SEQUENCE LISTING PATENT APPLICATION US/09/491,577

DATE: 02/15/2000
TIME: 14:09:10

Input Set: I491577.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

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1  <110> APPLICANT: Yale University
2      Carlson, John R.
3      Kim, Hunhyong
4      Clyne, Peter J.
5      Warr, Coral G.
6  <120> TITLE OF INVENTION: Novel Family of Odorant Receptor Genes in Drosophila
7  <130> FILE REFERENCE: 44574-5061-US
8  <140> CURRENT APPLICATION NUMBER: US/09/491,577
9  <141> CURRENT FILING DATE: 2000-01-25
10 <150> EARLIER APPLICATION NUMBER: US 60/117,132
11 <151> EARLIER FILING DATE: 1999-01-25
12 <160> NUMBER OF SEQ ID NOS: 112
13 <170> SOFTWARE: PatentIn Ver. 2.1
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15 <211> LENGTH: 767
16 <212> TYPE: DNA
17 <213> ORGANISM: Drosophila melanogaster
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20 <222> LOCATION: (1)..(765)
21 <223> OTHER INFORMATION: DOR 22A.2, coding region of NCBI Accession No.
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26         1             5             10             15
27     cgg gtt aag tcc cga gat gcc ttc gtt tac tta gat cgg gtg atg tgg      96
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29             20             25             30
30     tcc ttt ggc tgg aca gtg cct gaa aac aaa agg tgg gat cta cat tac      144
31     Ser Phe Gly Trp Thr Val Pro Glu Asn Lys Arg Trp Asp Leu His Tyr
32             35             40             45
33     aaa ctg tgg tca act ttc gtg aca ttg ttg ata ttt atc ctt ctg ccg      192
34     Lys Leu Trp Ser Thr Phe Val Thr Leu Leu Ile Phe Ile Leu Leu Pro
35             50             55             60
36     ata tcg gta agc gtt gag tat att cag cgg ttc aag acc ttc tcg gcg      240
37     Ile Ser Val Ser Val Glu Tyr Ile Gln Arg Phe Lys Thr Phe Ser Ala
38             65             70             75             80
39     ggt gag ttt ctt agc tca atc cag att ggc gtt aac atg tac gga agc      288
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41             85             90             95
42     agc ttt aaa agt tat ttg acc atg atg gga tat aag aag aga cag gag      336
43     Ser Phe Lys Ser Tyr Leu Thr Met Met Gly Tyr Lys Lys Arg Gln Glu
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PAGE: 2

RAW SEQUENCE LISTING PATENT APPLICATION US/09/491,577

DATE: 02/15/2000
TIME: 14:09:10

Input Set: I491577.RAW

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58      Val Asp Pro Glu Lys Gln Phe Tyr Ile Ser Ser Ile Ala Glu Val Ile
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64      Leu Ile Ser Met Val Ile Ala Arg Cys His Ile Thr Leu Leu Lys Gln
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66      cgc ctg cga aat cta cga tcg gaa cca gga agg acg gaa gat gag tac      720
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83      Lys Leu Trp Ser Thr Phe Val Thr Leu Leu Ile Phe Ile Leu Leu Pro
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86      65                                70                                75                                80
87      Gly Glu Phe Leu Ser Ser Ile Gln Ile Gly Val Asn Met Tyr Gly Ser
88      85                                90                                95
89      Ser Phe Lys Ser Tyr Leu Thr Met Met Gly Tyr Lys Lys Arg Gln Glu
90      100                                105                                110
91      Ala Lys Met Ser Leu Asp Glu Leu Asp Lys Arg Cys Val Cys Asp Glu
92      115                                120                                125
93      Glu Arg Thr Ile Val His Arg His Val Ala Leu Gly Asn Phe Cys Tyr
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PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/491,577

DATE: 02/15/2000
TIME: 14:09:10

Input Set: I491577.RAW

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97     Ser Phe Ile Met Lys Arg Ile His Ala Trp Arg Met Tyr Phe Pro Tyr
98                      165                      170                      175
99     Val Asp Pro Glu Lys Gln Phe Tyr Ile Ser Ser Ile Ala Glu Val Ile
100                      180                      185                      190
101     Leu Arg Gly Trp Ala Val Phe Met Asp Leu Cys Thr Asp Val Cys Pro
102                      195                      200                      205
103     Leu Ile Ser Met Val Ile Ala Arg Cys His Ile Thr Leu Leu Lys Gln
104                      210                      215                      220
105     Arg Leu Arg Asn Leu Arg Ser Glu Pro Gly Arg Thr Glu Asp Glu Tyr
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132     Val His Leu Asp Asn Leu Val Val Ala Leu Glu Ala Phe Cys Pro Gly
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134     acc acc aag gcg gtc tgc gtt ttg aag ctg tgg gtc ttc ttc cgc tcc      288
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137     aat cgc cgg tgg gcg gag ttg gtc cag cgc ctg cgg gct att ttg ctc      336
138     Asn Arg Arg Trp Ala Glu Leu Val Gln Arg Leu Arg Ala Ile Leu Leu
139                      100                      105                      110
140     agc ctg ttg ttg ctc agc tct ggc acg gcg aca aat gcc gcc ttc acc      384
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143     ttg caa ccg ctg att atg ggt ctc tac cgc tgg att gtg cag ctg cca      432
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PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/491,577

DATE: 02/15/2000
TIME: 14:09:10

Input Set: I491577.RAW

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150	Gln Pro Gly Val Phe Pro Leu Thr Tyr Val Leu Leu Thr Ala Ser Gly			
151	165 170 175			
152	gcc tgc acc gtt ttc gcc ttc agc ttc gtg gac gga ttc ttc att tgc	576		
153	Ala Cys Thr Val Phe Ala Phe Ser Phe Val Asp Gly Phe Phe Ile Cys			
154	180 185 190			
155	tcg tgc ctc tac atc tgc ggc gct ttc cgg ctg gtg cag cag gac att	624		
156	Ser Cys Leu Tyr Ile Cys Gly Ala Phe Arg Leu Val Gln Gln Asp Ile			
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158	cgc agg ata ttt gcc gat ttg cat ggc gtg gat gtg ttc acc gag gag	672		
159	Arg Arg Ile Phe Ala Asp Leu His Gly Val Asp Val Phe Thr Glu Glu			
160	210 215 220			
161	atg aac gcg gag gtg cgg cac aga ctg gcc caa gtt gtc gag cgg cac	720		
162	Met Asn Ala Glu Val Arg His Arg Leu Ala Gln Val Val Glu Arg His			
163	225 230 235 240			
164	aat gcg att atc gat ttc tgc acg gac cta aca cgc cag ttc acc gtt	768		
165	Asn Ala Ile Ile Asp Phe Cys Thr Asp Leu Thr Arg Gln Phe Thr Val			
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186	Phe Phe Thr Pro Ser Leu Pro Ala Leu Arg Ser Ile Leu Ser Thr Ala			
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193 <212> TYPE: PRT
194 <213> ORGANISM: Drosophila melanogaster

PAGE: 5

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PATENT APPLICATION US/09/491,577

DATE: 02/15/2000
TIME: 14:09:10

Input Set: I491577.RAW

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200 Gly Gly Gly Gly Arg Pro Trp His Ala His Leu Leu Phe Val Phe Ala
201 35 40 45
202 Phe Ala Met Val Val Val Gly Ala Val Gly Glu Val Ser Tyr Gly Cys
203 50 55 60
204 Val His Leu Asp Asn Leu Val Val Ala Leu Glu Ala Phe Cys Pro Gly
205 65 70 75 80
206 Thr Thr Lys Ala Val Cys Val Leu Lys Leu Trp Val Phe Phe Arg Ser
207 85 90 95
208 Asn Arg Arg Trp Ala Glu Leu Val Gln Arg Leu Arg Ala Ile Leu Leu
209 100 105 110
210 Ser Leu Leu Leu Ser Ser Gly Thr Ala Thr Asn Ala Ala Phe Thr
211 115 120 125
212 Leu Gln Pro Leu Ile Met Gly Leu Tyr Arg Trp Ile Val Gln Leu Pro
213 130 135 140
214 Gly Gln Thr Glu Leu Pro Phe Asn Ile Ile Leu Pro Ser Phe Ala Val
215 145 150 155 160
216 Gln Pro Gly Val Phe Pro Leu Thr Tyr Val Leu Leu Thr Ala Ser Gly
217 165 170 175
218 Ala Cys Thr Val Phe Ala Phe Ser Phe Val Asp Gly Phe Phe Ile Cys
219 180 185 190
220 Ser Cys Leu Tyr Ile Cys Gly Ala Phe Arg Leu Val Gln Gln Asp Ile
221 195 200 205
222 Arg Arg Ile Phe Ala Asp Leu His Gly Val Asp Val Phe Thr Glu Glu
223 210 215 220
224 Met Asn Ala Glu Val Arg His Arg Leu Ala Gln Val Val Glu Arg His
225 225 230 235 240
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227 245 250 255
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231 275 280 285
232 Ile Cys Tyr Ile Ile Ala Ala Leu Thr Gln Leu Phe Leu Tyr Cys Phe
233 290 295 300
234 Gly Gly Asn His Val Ser Glu Ser Ser Ala Ala Val Ala Asp Val Leu
235 305 310 315 320
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PAGE: 6

VERIFICATION SUMMARY
PATENT APPLICATION US/09/491,577

DATE: 02/15/2000
TIME: 14:09:10

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